

FES

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/720,934

DATE: 11/14/2001  
TIME: 14:05:23

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF3\11142001\I720934.raw

# by  
1.29.02

3 <110> APPLICANT: Korenberg, Julie R  
4 Chen, Xiao-Ning  
6 <120> TITLE OF INVENTION: ISOLATED SH3 GENES ASSOCIATED WITH MYELOPROLIFERATIVE  
7 DISORDERS AND LEUKEMIA, AND USES THEREOF  
9 <130> FILE REFERENCE: 2320-1-001PCT  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/720,934 ok  
C--> 12 <141> CURRENT FILING DATE: 2001-10-03  
14 <150> PRIOR APPLICATION NUMBER: 60/082,007  
15 <151> PRIOR FILING DATE: 1998-04-16  
17 <160> NUMBER OF SEQ ID NOS: 109  
19 <170> SOFTWARE: PatentIn Ver. 2.0  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 5199  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Homo sapiens  
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29 gtgagcggca ctgatttgct cctggggcgg cagcgcggac ccgcccggag atgaggcgctc 180  
30 gattagcaag gtaaaagtaa cagaaccatg gctcagtttc caacaccttt tgggtggcagc 240  
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32 ttaaaagcaa tatctggatt cattactggt gatcaagcta gaaacttttt ttttcaatct 360  
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35 tatcagctac cctctgcaact tccccctgtc atgaaacagc aaccagttgc tatttctagc 540  
36 gcaccagcat ttggtatggg aggtatcgcc agcatgccac cgcttacagc tgttgctcca 600  
37 gtgccaatgg gatccattcc agttgttgga atgtctccaa ccctagtatc ttctgttccc 660  
38 acagcagctg tgccccccct ggctaaccgg gctccccctg ttatacaacc tctgcctgca 720  
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41 gtggcagagt gggctgttcc tcagtcatac agactgaaat acaggcaatt attcaatagt 900  
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43 tcaagtttac cacaggctca gctggcttca atatggaatc tttctgacat tgatcaagat 1020  
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56 agcacaacaa aatctagaga gttgagaatt gccgaaatca cccatctaca gcaacaatta 1800  
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66 caccaagaac cagctaagcc agctgtccag gcacctggt ccactgcaga aaaaggtcca 2400
67 cttaccattt ctgcacagga aaatgtaaaa gtggtgtatt accgggact gtaccctttt 2460
68 gaatccagaa gccatgatga aatcactatc cagccaggag acatagtcac ggtggatgaa 2520
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72 gcagtaacct cttcagagcc ctccacgacc cctaataact gggccgactt cagctccacg 2760
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107 ttaaactacta gttggaagct ctcaataaaa atgcctgctg ctcacagcac agaaaatggg 4860
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111 tcacggatat gaatgtaaaa tatataaata tataaacctg aggatttaac aaatgtaaaa 5100
112 caaccttttg aattagttcc gagtatagat aattaaattt ttaaaacaaa agtaaaaaaa 5160
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115 &lt;210&gt; SEQ ID NO: 2

116 &lt;211&gt; LENGTH: 1143

117 &lt;212&gt; TYPE: PRT

118 &lt;213&gt; ORGANISM: Homo sapiens

120 &lt;400&gt; SEQUENCE: 2

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124 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe His Ser Leu
125           20           25           30
127 Lys Pro Ile Ser Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
128           35           40           45
130 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
131           50           55           60
133 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
134           65           70           75           80
136 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
137           85           90           95
139 Ala Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
140           100          105          110
142 Pro Ala Phe Gly Met Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala
143           115          120          125
145 Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro
146           130          135          140
148 Thr Leu Val Ser Ser Val Pro Thr Ala Ala Val Pro Pro Leu Ala Asn
149           145          150          155          160
151 Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala
152           165          170          175
154 Ala Thr Leu Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser
155           180          185          190
157 Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser
158           195          200          205
160 Val Pro Pro Val Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys
161           210          215          220
163 Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu
164           225          230          235          240
166 Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln
167           245          250          255
169 Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly
170           260          265          270
172 Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val
173           275          280          285
175 Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile

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178 Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Ile Ser Val Ile
179 305      310      315      320
181 Ser Ser Thr Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Val Leu Glu
182      325      330      335
184 Asp Glu Gln Gln Gln Leu Glu Lys Lys Leu Pro Val Thr Phe Glu Asp
185      340      345      350
187 Lys Lys Arg Glu Asn Phe Glu Arg Gly Asn Leu Glu Leu Glu Lys Arg
188      355      360      365
190 Arg Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala
191      370      375      380
193 Gln Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu
194 385      390      395      400
196 Gln Glu Arg Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln
197      405      410      415
199 Arg Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu
200      420      425      430
202 Arg Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu
203      435      440      445
205 Trp Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu
206      450      455      460
208 Gln Glu Asp Ile Val Val Leu Lys Ala Lys Lys Lys Thr Leu Glu Phe
209 465      470      475      480
211 Glu Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu
212      485      490      495
214 Gln Asp Ile Arg Cys Arg Leu Thr Thr Gln Arg Gln Glu Ile Glu Ser
215      500      505      510
217 Thr Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln
218      515      520      525
220 Gln Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu
221      530      535      540
223 Lys Gln Ile Leu Asn Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu
224 545      550      555      560
226 His Arg Asp Ser Leu Val Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu
227      565      570      575
229 Leu Ala Arg Gln His Leu Arg Asp Gln Leu Asp Glu Val Glu Lys Glu
230      580      585      590
232 Thr Arg Ser Lys Leu Gln Glu Ile Asp Ile Phe Asn Asn Gln Leu Lys
233      595      600      605
235 Glu Leu Arg Glu Ile His Asn Lys Gln Gln Leu Gln Lys Gln Lys Ser
236      610      615      620
238 Met Glu Ala Glu Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ile Ile
239 625      630      635      640
241 Glu Leu Glu Lys Gln Lys Glu Glu Ala Gln Arg Arg Ala Gln Glu Arg
242      645      650      655
244 Asp Lys Gln Trp Leu Glu His Val Gln Gln Glu Asp Glu His Gln Arg
245      660      665      670
247 Pro Arg Lys Leu His Glu Glu Glu Lys Leu Lys Arg Glu Glu Ser Val
248      675      680      685

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254 705      710      715      720
256 Gln Ala Pro Trp Ser Thr Ala Glu Lys Gly Pro Leu Thr Ile Ser Ala
257      725      730      735
259 Gln Glu Asn Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu
260      740      745      750
262 Ser Arg Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met
263      755      760      765
265 Val Asp Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu
266      770      775      780
268 Lys Gly Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro
269 785      790      795      800
271 Glu Asn Glu Val Pro Ala Pro Val Lys Pro Val Thr Asp Ser Thr Ser
272      805      810      815
274 Ala Pro Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Ala
275      820      825      830
277 Val Thr Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe
278      835      840      845
280 Ser Ser Thr Trp Pro Thr Ser Thr Asn Glu Lys Pro Glu Thr Asp Asn
281      850      855      860
283 Trp Asp Ala Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly
284 865      870      875      880
286 Gln Leu Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser
287      885      890      895
289 Ser Pro Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln
290      900      905      910
292 Ala Gln Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn
293      915      920      925
295 Phe Asn Lys Asn Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp
296      930      935      940
298 Trp Phe Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr
299 945      950      955      960
301 Val Lys Leu Ile Ser Gly Pro Ile Arg Lys Ser Thr Ser Met Asp Ser
302      965      970      975
304 Gly Ser Ser Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala
305      980      985      990
307 Ala Lys Pro Val Val Ser Gly Glu Glu Ile Ala Gln Val Ile Ala Ser
308      995      1000      1005
310 Tyr Thr Ala Thr Gly Pro Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu
311      1010      1015      1020
313 Ile Leu Ile Arg Lys Lys Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu
314 1025      1030      1035      1040
316 Gln Ala Arg Gly Lys Lys Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr
317      1045      1050      1055
319 Val Lys Leu Leu Ser Pro Gly Thr Ser Lys Ile Thr Pro Thr Glu Pro
320      1060      1065      1070
322 Pro Lys Ser Thr Ala Leu Ala Ala Val Cys Gln Val Ile Gly Met Tyr

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